glutamic acid, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, and valine. --

--3. (Amended) The soluble CTLA4 mutant molecule of claim 1, wherein the extracellular domain of CTLA4 comprises a mutation in a region S25-R33 of CTLA4 of Figure 3 (SEQ ID NO.: 2, at positions 51-59), and wherein the mutation is a substitution of alanine at position +29 of Figure 3 (SEQ ID NO.: 2, at position 55) with any of arginine, asparagine, aspartic acid, cysteine, glutamine, glutamic acid, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, or valine. --

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--4. (Amended) The soluble CTLA4 mutant molecule of claim 1, wherein the extracellular domain of CTLA4 comprises one or more mutations in a region S25-R33 of CTLA4 of Figure 3 (SEQ ID NO.: 2, at positions 51-59), and wherein the mutation is a substitution of any amino acid beginning with threonine at position +30 of Figure 3 (SEQ ID NO.: 2, at position 56) and ending with arginine at position +33 of Figure 3 (SEQ ID NO.: 2, at position 59) with a different amino acid selected from alanine, arginine, asparagine, aspartic acid, cysteine, glutamine, glutamic acid, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, and valine.--

--5. (Amended) The soluble CTLA4 mutant molecule of claim 1, wherein the extracellular domain of CTLA4 comprises one or more mutations in a region E95-G107 of CTLA4 of Figure 3 (SEQ ID NO.: 2, at positions 121-133), and wherein the mutation is a substitution of any amino acid beginning with glutamic acid at position +95 of Figure 3 (SEQ ID NO.: 2, at position 121) and ending with leucine at position +96 of Figure 3 (SEQ ID NO.: 2, at position 122) with a different amino acid selected from alanine, arginine, asparagine, aspartic acid, cysteine, glutamine, glutamic acid, glycine, histidine, isoleucine, leucine, lysine,

methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, and valine. --

--6. (Amended) The soluble CTLA4 mutant molecule of claim 1, wherein the extracellular domain of CTLA4 comprises one or more mutations in a region E95-G107 of CTLA4 of Figure 3 (SEQ ID NO.: 2, at positions 121-133), and wherein the mutation is a substitution of any amino acid beginning with methionine at position +97 of Figure 3 (SEQ ID NO.: 2, at position 123) and ending with tyrosine at position +103 of Figure 3 (SEQ ID NO.: 2, at position 129) with a different amino acid selected from alanine, arginine, asparagine, aspartic acid, cysteine, glutamine, glutamic acid, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, and valine. --

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--7. (Amended) The soluble CTLA4 mutant molecule of claim 6, wherein the mutation is a substitution of tyrosine at position +103 of Figure 3 (SEQ ID NO.: 2, at position 129) with a different amino acid selected from a group consisting of arginine, asparagine, aspartic acid, cysteine, glutamine, glutamic acid, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, and valine. --

--8. (Amended) The soluble CTLA4 mutant molecule of claim 1, wherein the extracellular domain of CTLA4 comprises one or more mutations in a region E95-G107 of CTLA4 of Figure 3 (SEQ ID NO.: 2, at positions 121-133), and wherein the mutation is a substitution of any amino acid beginning with leucine at position +104 of Figure 3 (SEQ ID NO.: 2, at position 130) and ending with glycine at position +107 of Figure 3 (SEQ ID NO.: 2, at position 133) with a different amino acid selected from alanine, arginine, asparagine, aspartic acid, cysteine, glutamine, glutamic acid, glycine, histidine, isoleucine, leucine, lysine,

methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, and valine. --

--9. (Amended) The soluble CTLA4 mutant molecule of claim 1, wherein the extracellular domain of CTLA4 comprises one or more mutations in a region N108-I115 of CTLA4 of Figure 3 (SEQ ID NO.: 2, at positions 134-141), and wherein the mutation is a substitution of any amino acid beginning with asparagine at position +108 of Figure 3 (SEQ ID NO.: 2, at position 134) and ending with isoleucine at position +115 of Figure 3 (SEQ ID NO.: 2, at position 141) with a different amino acid selected from a group consisting of alanine, arginine, asparagine, aspartic acid, cysteine, glutamine, glutamic acid, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, and valine. --

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Concluded

--20. (Amended) The method of claim 19, wherein the soluble CTLA4 mutant molecule is any of L104EA29L (SEQ ID NO.: 16), L104EA29T (SEQ ID NO.: 18), or L104EA29W (SEQ ID NO.: 20).

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REMARKS

Claims 1-25 were pending. Applicants have canceled claim 10 without prejudice. Additionally, Applicants have amended claims 2-9, and 20. Accordingly, claims 1-9, and 11-25 are presently pending.

The amendments to claims 2-9, and 20 are made to provide SEQ ID NOs in the claims and correct typographical errors. Additionally, claim 9 is amended to incorporate the contents of claim 10, and claim 10 is canceled. The amendments to correct typographical errors and incorporate SEQ ID NOs in the claims do not introduce any new matter and